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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373

FORMALITIES LETTER



OC000000007141372

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Date Mailed: 11/30/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

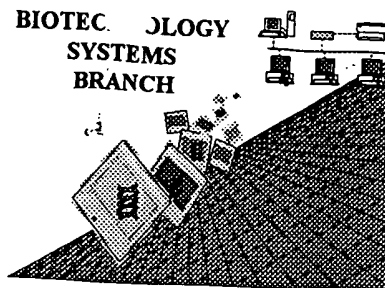
- For Rules Interpretation, call (703) 308-4216
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PART 3 - OFFICE COPY

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,881A
Source: OIPK
Date Processed by STIC: 10/15/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001

TIME: 15:47:14

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

3 <110> APPLICANT: Scott, Fred W.
 5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
 7 <130> FILE REFERENCE: 18617.0016
 9 <140> CURRENT APPLICATION NUMBER: US 09/873,881A
 10 <141> CURRENT FILING DATE: 2001-06-04
 12 <150> PRIOR APPLICATION NUMBER: US 08/552,369
 13 <151> PRIOR FILING DATE: 1995-11-03
 15 <160> NUMBER OF SEQ ID NOS: 19

Does Not Comply
 Corrected Diskette Needed

pp 1,3-4

ERRORED SEQUENCES

932 <210> SEQ ID NO: 19
 933 <211> LENGTH: 1979
 934 <212> TYPE: DNA
 935 <213> ORGANISM: feline leukemia virus
 937 <220> FEATURE:
 938 <223> OTHER INFORMATION:
 940 <400> SEQUENCE: 19

941	accaccaatc aagacctctc ggacagcccc agctcagacg atccatcaag	50
943	atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc	95
944	Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu	
945	1 5 10 15	
947	tgc tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140
948	Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp	
949	20 25 30	
951	ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185
952	Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr	
953	35 40 45	
955	tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230
956	Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr	
957	50 55 60	
959	tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275
960	Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val	
961	65 70 75	
963	gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320
964	Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu	
965	80 85 90	
967	aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365
968	Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys	
W--> 969	95 100 105	
971	tat gga tgt aaa act aca gat aga aaa cag caa cag aca tac	410
972	Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr	
973	110 115 120	
975	ccc ttt tac gtc tgc ccc gga cat gcc ccc tgc ttg ggg cca aag	455
976	Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys	
W--> 977	125 130 135	

numbers are
 in bold print
 due to error
 above - apostrophe

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001

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Input Set : A:\corrected sequence listing for Scott et al
 Output Set: N:\CRF3\10152001\I873881A.raw

979 gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg 500
 980 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
 W--> 981 140 145 150
 983 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca 545
 984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
 W--> 985 155 160 165
 987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 590
 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
 W--> 989 170 175 180
 991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 635
 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
 W--> 993 185 190 195
 995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 680
 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
 W--> 997 200 205 210
 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 725
 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
 W--> 1001 215 220 225
 1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac 770
 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
 W--> 1005 230 235 240
 1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca 815
 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
 W--> 1009 245 250 255
 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 860
 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
 W--> 1013 260 265 270
 1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905
 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
 W--> 1017 275 280 285
 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950
 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
 W--> 1021 290 295 300
 1023 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc 995
 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
 W--> 1025 305 310 315
 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040
 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
 W--> 1029 320 325 330
 1031 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act 1085
 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
 W--> 1033 335 340 345
 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130
 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
 W--> 1037 350 355 360
 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175
 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
 W--> 1041 365 370 375
 1043 aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac 1220

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Input Set : A:\corrected sequence listing for Scott et al

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	1044	Thr	Gln	Gln	Gly	His	Thr	Gly	Ala	His	Tyr	Leu	Ala	Ala	Pro	Asn	
W-->	1045					380					385					390	
	1047	ggc	acc	tat	tgg	gcc	tgt	aac	act	gga	ctc	acc	cca	tgc	att	tcc	1265
	1048	Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser	
W-->	1049					395					400					405	
	1051	atg	gcg	gtg	ctc	aat	tgg	acc	tct	gat	ttt	tgt	gtc	tta	atc	gaa	1310
	1052	Met	Ala	Val	Leu	Asn	Trp	Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu	
W-->	1053					410					415					420	
	1055	tta	tgg	ccc	aga	gtg	act	tac	cat	caa	ccc	gaa	tat	gtg	tac	aca	1355
	1056	Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr	
W-->	1057					425					430					435	
	1059	cat	ttt	gcc	aaa	gct	gtc	agg	ttc	cga	aga	gaa	cca	ata	tca	cta	1400
	1060	His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Arg	Glu	Pro	Ile	Ser	Leu	
W-->	1061					440					445					450	
	1063	acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcc	1445
	1064	Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	
W-->	1065					455					460					465	
	1067	gcg	ggg	gtc	gga	aca	ggg	act	aaa	gcc	ctc	ctt	gaa	aca	gcc	cag	1490
	1068	Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	
W-->	1069					470					475					480	
	1071	ttc	aga	caa	cta	caa	atg	gcc	atg	cac	aca	gac	atc	cag	gcc	cta	1535
	1072	Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	
W-->	1073					485					490					495	
	1075	gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580
	1076	Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	
W-->	1077					500					505					510	
	1079	gaa	gta	gtc	tta	caa	aac	aga	cgg	ggc	cta	gat	att	cta	ttc	tta	1625
	1080	Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	
W-->	1081					515					520					525	
	1083	caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc	1670
	1084	Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	
W-->	1085					530					535					540	
	1087	tat	gcg	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta	1715
	1088	Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	
W-->	1089					545					550					555	
	1091	aga	gaa	aga	cta	aaa	cag	cgg	caa	caa	ctg	ttt	gac	tcc	caa	cag	1760
	1092	Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	
W-->	1093					560					565					570	
	1095	gga	tgg	ttt	gaa	gga	tgg	ttc	aac	aag	tcc	ccc	tgg	ttt	aca	acc	1805
	1096	Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	
W-->	1097					575					580					585	
	1099	cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att	1850
	1100	Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile	
W-->	1101					590					595					600	
	1103	ctc	ctc	ttc	ggc	cca	tgc	atc	ctt	aac	cga	tta	gta	caa	ttc	gta	1895
	1104	Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val	
W-->	1105					605					610					615	
	1107	aaa	gac	aga	ata	tct	gtg	gta	cag	gct	tta	att	tta	acc	caa	cag	1940
W-->	1108	Lys	Asp	<u>Arg</u>	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln	

invalid

↑

RAW SEQUENCE LISTING

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Input Set : A:\corrected sequence listing for Scott et al

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W--> 1109 620 625 630
1111 tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979
1112 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
W--> 1113 635 640
E--> 1117 bFLOdOcs:589477_1 (cm%d01)

Delete

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:16

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

L:21 M:283 W: Missing Blank Line separator, <220> field identifier
 L:912 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1001 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
 L:1117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1995 SEQ:19
 L:1117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
 L:1117 M:112 C: (48) String data converted to lower case,
 L:1117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1995 SEQ:19